

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/540,245  
DATE: 08/21/2000  
TIME: 12:44:22

Input Set : A:\09540245.txt  
Output Set : N:\CRF3\08212000\I540245.raw

5 <110> APPLICANT: Goodman, Corey  
7 Kid, Thomas  
9 Brose, Katja  
11 Tessier-Lavigne, Marc  
15 <120> TITLE OF INVENTION: Modulating Robo: Ligand Interactions  
19 <130> FILE REFERENCE: B98-031-3  
23 <140> CURRENT APPLICATION NUMBER: 09/540,245  
25 <141> CURRENT FILING DATE: 2000-03-31  
29 <150> PRIOR APPLICATION NUMBER: 09/191,647  
31 <151> PRIOR FILING DATE: 1998-11-13  
35 <150> PRIOR APPLICATION NUMBER: 60/081,057  
37 <151> PRIOR FILING DATE: 1998-04-07  
41 <160> NUMBER OF SEQ ID NOS: 14  
45 <170> SOFTWARE: PatentIn Ver. 2.0  
49 <210> SEQ ID NO: 1  
51 <211> LENGTH: 4758  
53 <212> TYPE: DNA  
55 <213> ORGANISM: human  
59 <220> FEATURE:  
61 <221> NAME/KEY: CDS  
63 <222> LOCATION: (1)..(4575)  
67 <400> SEQUENCE: 1  
69 atg cgc ggc gtt ggc tgg cag atg ctg tcc ctg tgc ctg ggg tta gtg 48  
71 Met Arg Gly Val Gly Trp Gln Met Leu Ser Leu Gly Leu Val  
73 1 5 10 15  
77 ctg gcg atc ctg aac aag gtg gca ccg cag gcg tgc ccg gcg cag tgc 96  
79 Leu Ala Ile Leu Asn Lys Val Ala Pro Gln Ala Cys Pro Ala Gln Cys  
81 20 25 30  
85 tct tgc tgc ggc agc aca gtg gac tgt cac ggg ctg gcg ctg cgc agc 144  
87 Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser  
89 35 40 45  
93 gtg ccc agg aat atc ccc cgc aac acc gag aga ctg gat tta aat gga 192  
95 Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly  
97 50 55 60  
101 aat aac atc aca aga att acg aag aca gat ttt gct ggt ctt aga cat 240  
103 Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His  
105 65 70 75 80  
109 cta aga gtt ctt cag ctt atg gag aat aag att agc acc att gaa aga 288  
111 Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg  
113 85 90 95  
117 gga gca ttc cag gat ctt aaa gaa cta gag aga ctg cgt tta aac aga 336  
119 Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg  
121 100 105 110  
125 aat cac ctt cag ctg ttt cct gag ttg ctg ttt ctt ggg act gcg aag 384  
127 Asn His Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys  
129 115 120 125  
133 cta tac agg ctt gat ctc agt gaa aac caa att cag gca atc cca agg 432

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```

135 Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg
137      130      135      140
141 aaa gct ttc cgt ggg gca gtt gac ata aaa aat ttg caa ctg gat tac 480
143 Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr
145 145      150      155      160
149 aac cag atc agc tgt att gaa gat ggg gca ttc agg gct ctc cgg gac 528
151 Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp
153      165      170      175
157 ctg gaa gtg ctc act ctc aac aat aac att act aga ctt tct gtg 576
159 Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser Val
161      180      185      190
165 gca agt ttc aac cat atg cct aaa ctt agg act ttt cga ctg cat tca 624
167 Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser
169      195      200      205
173 aac aac ctg tat tgt gac tgc cac ctg gcc tgg ctc tcc gac tgg ctt 672
175 Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu
177      210      215      220
181 cgc aaa agg cct cgg gtt ggt ctg tac act cag tgt atg ggc ccc tcc 720
183 Arg Lys Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser
185 225      230      235      240
189 cac ctg aga ggc cat aat gta gcc gag gtt caa aaa cga gaa ttt gtc 768
191 His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val
193      245      250      255
197 tgc agt gat gag gaa gaa ggt cac cag tca ttt atg gct cct tct tgt 816
199 Cys Ser Asp Glu Glu Gly His Gln Ser Phe Met Ala Pro Ser Cys
201      260      265      270
205 agt gtt ttg cac tgc cct gcc gcc tgt acc tgt agc aac aat atc gta 864
207 Ser Val Leu His Cys Pro Ala Ala Cys Thr Cys Ser Asn Asn Ile Val
209      275      280      285
213 gac tgt cgt ggg aaa ggt ctc act gag atc ccc aca aat ctt cca gag 912
215 Asp Cys Arg Gly Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu
217      290      295      300
221 acc atc aca gaa ata cgt ttg gaa cag aac aca atc aaa gtc atc cct 960
223 Thr Ile Thr Glu Ile Arg Leu Glu Gln Asn Thr Ile Lys Val Ile Pro
225 305      310      315      320
229 cct gga gct ttc tca cca tat aaa aag ctt aga cga att gac ctg agc 1008
231 Pro Gly Ala Phe Ser Pro Tyr Lys Lys Leu Arg Arg Ile Asp Leu Ser
233      325      330      335
237 aat aat cag atc tct gaa ctt gca cca gat gct ttc caa gga cta cgc 1056
239 Asn Asn Gln Ile Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg
241      340      345      350
245 tct ctg aat tca ctt gtc ctc tat gga aat aaa atc aca gaa ctc ccc 1104
247 Ser Leu Asn Ser Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro
249      355      360      365
253 aaa agt tta ttt gaa gga ctg ttt tcc tta cag ctc cta tta ttg aat 1152
255 Lys Ser Leu Phe Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Asn
257      370      375      380
261 gcc aac aag ata aac tgc ctt cgg gta gat gct ttt cag gat ctc cac 1200
263 Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His

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```

265 385          390          395          400
269 aac ttg aac ctt ctc tcc cta tat gac aac aag ctt cag acc atc gcc 1248
271 Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala
273          405          410          415
277 aag ggg acc ttt tca cct ctt cgg gcc att caa act atg cat ttg gcc 1296
279 Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala
281          420          425          430
285 cag aac ccc ttt att tgt gac tgc cat ctc aag tgg cta gcg gat tat 1344
287 Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr
289          435          440          445
293 ctc cat acc aac ccg att gag acc agt ggt gcc cgt tgc acc agc ccc 1392
295 Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro
297          450          455          460
301 cgc cgc ctg gca aac aaa aga att gga cag atc aaa agc aag aaa ttc 1440
303 Arg Arg Leu Ala Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe
305 465          470          475          480
309 cgt tgt tca ggt aca gaa gat tat cga tca aaa tta agt gga gac tgc 1488
311 Arg Cys Ser Gly Thr Glu Asp Tyr Arg Ser Lys Leu Ser Gly Asp Cys
313          485          490          495
317 ttt gcg gat ctg gct tgc cct gaa aag tgt cgc tgt gaa gga acc aca 1536
319 Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys Glu Gly Thr Thr
321          500          505          510
325 gta gat tgc tct aat caa aag ctc aac aaa atc ccg gag cac att ccc 1584
327 Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro Glu His Ile Pro
329          515          520          525
333 cag tac act gca gag ttg cgt ctc aat aat aat gaa ttt acc gtg ttg 1632
335 Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu Phe Thr Val Leu
337          530          535          540
341 gaa gcc aca gga atc ttt aag aaa ctt cct caa tta cgt aaa ata aac 1680
343 Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu Arg Lys Ile Asn
345 545          550          555          560
349 ttt agc aac aat aag atc aca gat att gag gag gga gca ttt gaa gga 1728
351 Phe Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly Ala Phe Glu Gly
353          565          570          575
357 gca tct ggt gta aat gaa ata ctt ctt acg agt aat cgt ttg gaa aat 1776
359 Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn Arg Leu Glu Asn
361          580          585          590
365 gtg cag cat aag atg ttc aag gga ttg gaa agc ctc aaa act ttg atg 1824
367 Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu Lys Thr Leu Met
369          595          600          605
373 ttg aga agc aat cga ata acc tgt gtg ggg aat gac agt ttc ata gga 1872
375 Leu Arg Ser Asn Arg Ile Thr Cys Val Gly Asn Asp Ser Phe Ile Gly
377          610          615          620
381 ctc agt tct gtg cgt ttg ctt tct ttg tat gat aat caa att act aca 1920
383 Leu Ser Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn Gln Ile Thr Thr
385 625          630          635          640
389 gtt gca cca ggg gca ttt gat act ctc cat tct tta tct act cta aac 1968
391 Val Ala Pro Gly Ala Phe Asp Thr Leu His Ser Leu Ser Thr Leu Asn
393          645          650          655

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397 ctc ttg gcc aat cct ttt aac tgt aac tgc tac ctg gct tgg ttg gga 2016
399 Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys Tyr Leu Ala Trp Leu Gly
401          660          665          670
405 gag tgg ctg aga aag aag aga att gtc acg gga aat cct aga tgt caa 2064
407 Glu Trp Leu Arg Lys Lys Arg Ile Val Thr Gly Asn Pro Arg Cys Gln
409          675          680          685
413 aaa cca tac ttc ctg aaa gaa ata ccc atc cag gat gtg gcc att cag 2112
415 Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala Ile Gln
417          690          695          700
421 gac ttc act tgt gat gac gga aat gat gac aat agt tgc tcc cca ctt 2160
423 Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser Cys Ser Pro Leu
425 705          710          715          720
429 tct cgc tgt cct act gaa tgt act tgc ttg gat aca gtc gtc cga tgt 2208
431 Ser Arg Cys Pro Thr Glu Cys Thr Cys Leu Asp Thr Val Val Arg Cys
433          725          730          735
437 agc aac aag ggt ttg aag gtc ttg ccg aaa ggt att cca aga gat gtc 2256
439 Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile Pro Arg Asp Val
441          740          745          750
445 aca gag ttg tat ctg gat gga aac caa ttt aca ctg gtt ccc aag gaa 2304
447 Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu
449          755          760          765
453 ctc tcc aac tac aaa cat tta aca ctt ata gac tta agt aac aac aga 2352
455 Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg
457          770          775          780
461 ata agc acg ctt tct aat cag agc ttc agc aac atg acc cag ctc ctc 2400
463 Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu
465 785          790          795          800
469 acc tta att ctt agt tac aac cgt ctg aga tgt att cct cct cgc acc 2448
471 Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr
473          805          810          815
477 ttt gat gga tta aag tct ctt cga tta ctt tct cta cat gga aat gac 2496
479 Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp
481          820          825          830
485 att tct gtt gtg cct gaa ggt gct ttc aat gat ctt tct gca tta tca 2544
487 Ile Ser Val Val Pro Glu Gly Ala Phe Asn Asp Leu Ser Ala Leu Ser
489          835          840          845
493 cat cta gca att gga gcc aac cct ctt tac tgt gat tgt aac atg cag 2592
495 His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln
497          850          855          860
501 tgg tta tcc gac tgg gtg aag tcg gaa tat aag gag cct gga att gct 2640
503 Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala
505 865          870          875          880
509 cgt tgt gct ggt cct gga gaa atg gca gat aaa ctt tta ctc aca act 2688
511 Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr
513          885          890          895
517 ccc tcc aaa aaa ttt acc tgt caa ggt cct gtg gat gtc aat att cta 2736
519 Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp Val Asn Ile Leu
521          900          905          910
525 gct aag tgt aac ccc tgc cta tca aat ccg tgt aaa aat gat ggc aca 2784

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```

527 Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr
529          915          920          925
533 tgt aat agt gat cca gtt gac ttt tac cga tgc acc tgt cca tat ggt 2832
535 Cys Asn Ser Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly
537          930          935          940
541 ttc aag ggg cag gac tgt gat gtc cca att cat gcc tgc atc agt aac 2880
543 Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Ile Ser Asn
545 945          950          955          960
549 cca tgt aaa cat gga gga act tgc cac tta aag gaa gga gaa gaa gat 2928
551 Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu Gly Glu Glu Asp
553          965          970          975
557 gga ttc tgg tgt att tgt gct gat gga ttt gaa gga gaa aat tgt gaa 2976
559 Gly Phe Trp Cys Ile Cys Ala Asp Gly Phe Glu Gly Glu Asn Cys Glu
561          980          985          990
565 gtc aac gtt gat gat tgt gaa gat aat gac tgt gaa aat aat tct aca 3024
567 Val Asn Val Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr
569          995          1000          1005
573 tgt gtc gat ggc att aat aac tac aca tgc ctt tgc cca cct gag tat 3072
575 Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr
577          1010          1015          1020
581 aca ggt gag ttg tgt gag gag aag ctg gac ttc tgt gcc cag gac ctg 3120
583 Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu
585 1025          1030          1035          1040
589 aac ccc tgc cag cac gat tca aag tgc atc cta act cca aag gga ttc 3168
591 Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe
593          1045          1050          1055
597 aaa tgt gac tgc aca cca ggg tac gta ggt gaa cac tgc gac atc gat 3216
599 Lys Cys Asp Cys Thr Pro Gly Tyr Val Gly Glu His Cys Asp Ile Asp
601          1060          1065          1070
605 ttt gac gac tgc caa gac aac aag tgt aaa aac gga gcc cac tgc aca 3264
607 Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr
609          1075          1080          1085
613 gat gca gtg aac ggc tat acg tgc ata tgc ccc gaa ggt tac agt ggc 3312
615 Asp Ala Val Asn Gly Tyr Thr Cys Ile Cys Pro Glu Gly Tyr Ser Gly
617          1090          1095          1100
621 ttg ttc tgt gag ttt tct cca ccc atg gtc ctc cct cgt acc agc ccc 3360
623 Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Pro Arg Thr Ser Pro
625 1105          1110          1115          1120
629 tgt gat aat ttt gat tgt cag aat gga gct cag tgt atc gtc aga ata 3408
631 Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Val Arg Ile
633          1125          1130          1135
637 aat gag cca ata tgt cag tgt ttg cct ggc tat cag gga gaa aag tgt 3456
639 Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Gln Gly Glu Lys Cys
641          1140          1145          1150
645 gaa aaa ttg gtt agt gtg aat ttt ata aac aaa gag tct tat ctt cag 3504
647 Glu Lys Leu Val Ser Val Asn Phe Ile Asn Lys Glu Ser Tyr Leu Gln
649          1155          1160          1165
653 att cct tca gcc aag gtt cgg cct cag acg aac ata aca ctt cag att 3552
655 Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\09540245.txt

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L:1615 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5  
L:1615 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:1615 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:1615 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:1615 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5  
L:1627 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5  
L:1627 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:1627 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:1627 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
M:340 Repeated in SeqNo=5  
L:2278 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:2278 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:2278 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:2278 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:2278 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8  
L:2320 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:2320 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:2320 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:2320 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
M:340 Repeated in SeqNo=8  
L:2332 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:2332 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:2332 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:2332 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8